

SEQUENCE LISTING

<110> Carter Holt Harvey Limited
 Tasman Biotechnology Limited
 Michigan Technological University
 Podila, Gopi Krishna
 Liu, Jun-Jun
 Karnosky, David F

<120> Plants Having Modified Reproductive Activity

<130> 25635 MRB

<140>

<141>

<150> NZ334715

<151> 1999-03-17

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 1320

<212> DNA

<213> Pinus radiata

<400> 1

```

aaactcgaca gcaaatatga tttagattat gacctagaaa taagcatagc attaaagcat 60
atacataaca agcgggtgata tactctgact gccactgtac ttgaggaaaag gtagtggact 120
ctgctcaggt acattagttt ggtaagggtt gcttggtctt tgggtaatat gagaagtaaa 180
gaagtaaaag gtatttgact ctagtcaagt acattggatt gcctttgtcg gggcttggat 240
ggcttgggtt cgtgtgagaa gccaacaatt tataagaaat atataaaata aaaaataaaa 300
aaatttaagt gttggaagtg aaaacgggtg ggcagaaata tacacagaag agtactttaa 360
caatgcgcaa ccaaggcaga ttcacaactt gatttctgga cctcgaatac gagataatgg 420
tggttaagaaa taaaggaaga gtggagtgc tttgaaaatg aatggagagc gcacaaaatg 480
gaggacgaat aaatgaaata taatgcaaga gtgcatttcc ctattatttc cagaaatgta 540
tatgtggggt cggcattcac atgggcgtcg cattcagggg gtgtcatagc ggtcctttga 600
ttgcagtgtg ggagttgcaa catgtaccaa caaatccatt catcccaaaa cctaaattta 660
tcctctccat tactattacc tacacctata cctagtaa atgtcctgcc ttgtaactcc 720
tccactgcct gcacacgtct tagtcaatcc atctgccttc aaataggcat tattttgttc 780
tttcccctcc gactgaaagg ctatcgaccg accgaccgct catcttcttc ttctgcgcaa 840
ttttttctgc tggatcatca tcattaccat catcgccatc cccaccatca tcatcatgat 900
ggtatctcta tctctccctg gcaatcgatt gtagaggaaa ggaagaggga aggggcatat 960
gtattgatca acctaccoga aaaaacaatc tgatcagccc tgctcaatct tgcttataaa 1020
tctcttatcc actgttcaat cattcaggtt tcttcccact ttcaagcaaa ggcgcccga 1080
ttggcgtgt tcttagattt tcaggtactt aaatggacaa tattccccac ctgaagccgt 1140

```

tctgaaaaag atttgtttgt agaaacaaac gattgtaata tttgcttaag ttgagcttaa 1200
 ggggttttgg acctaacttg ccttgttggtt atttgtttct cagaactcgg gctgcgtcca 1260
 actgtaggaa cgaaccagca caaggggttg cagcttttgc tgttgctgtt gcgcccattg 1320

<210> 2

<211> 1401

<212> DNA

<213> Pinus radiata

<400> 2

aaactcgaca gcaaatatga tttagattat gacctagaaa taagcatagc attaaagcat 60
 atacataaca agcgggtgata tactctgact gccactgtac ttgaggaaag gtagtggact 120
 ctgctcaggt acattagttt ggtaagggtt gcttggcttc tgggtaatat gagaagtaaa 180
 gaagtaaaag gtatttgact ctagtcaagt acattggatt gcctttgtcg gggcttggat 240
 ggcttgggtt cgtgtgagaa gccacaatt tataagaaat atataaaaata aaaaataaaa 300
 aaattttaagt gttggaagtg aaaacgggtg ggcagaaata tacacagaag agtactttaa 360
 caatgcgcaa ccaaggcaga ttcacaactt gatttctgga cctcgaatac gagataatgg 420
 tggtaagaaa taaaggaaga gtggagtgc tttgaaaatg aatggagagc gcacaaaatg 480
 gaggacgaat aaatgaaata taatgcaaga gtgcatttcc ctattatttc cagaaatgta 540
 tatgtggggt cggcattcac atgggcgtcg cattcagggg gtgtcatagc ggtcctttga 600
 ttgcagtgtg ggagttgcaa catgtaccaa caaatccatt catcccaaaa cctaaattta 660
 tcctctccat tactattacc tacacctata cctagtaaat atgtcctgcc ttgtaactcc 720
 tccactgcct gcacacgtct tagtcaatcc atctgccttc aaataggcat tattttgttc 780
 tttccctcc gactgaaagg ctatcgaccg accgaccgct catcttcttc ttctgcgcaa 840
 tttttctgc tggatcatca tcattaccat catcgccatc cccaccatca tcatcatgat 900
 ggtatctcta tctctccctg gcaatcgatt gtagaggaaa ggaagaggga aggggcatat 960
 gtattgatca acctaccga aaaaacaatc tgatcagccc tgcataatct tgcttataaa 1020
 tctcttatcc actgttcaat cattcagggt tcttccact ttcaagcaaa ggcgcccga 1080
 ttggccgtgt tcttagattt tcaggtaact aaatggacaa tattccccac ctgaagccgt 1140
 tctgaaaaag atttgtttgt agaaacaaac gattgtaata tttgcttaag ttgagcttaa 1200
 ggggttttgg acctaacttg ccttgttggtt atttgtttct cagaactcgg gctgcgtcca 1260
 actgtaggaa cgaaccagca caaggggttg cagcttttgc tgttgctgtt gcgcccattg 1320
 cttttggact ggtattagta gttgcagctt tgttttgcac acgctgtgag gatctgtgcg 1380
 cggaaatttt gtgtacaaat c 1401

<210> 3

<211> 909

<212> DNA

<213> Pinus radiata

<220>

<221> CDS

<222> (1)..(669)

<223> Pinus radiata MADS box protein mRNA, complete cds

<300>

<301> Jun-Jun, Liu

Podila, G K.

<302> Not applicable

<303> Direct submission

<304> -

<305> -

<306> ---

<307> 1997-09-09

<308> Genbank AF023615

<309> 1999-01-26

<313> 1 TO 909

<400> 3

atg ggt cgt ggg aag att gag ata aag agg att gaa aat act acg aac	48
Met Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn	
1 5 10 15	

cga cag gtc act ttc tgc aag cgc cga aat ggt tta tta aag aag gcg	96
Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala	
20 25 30	

tat gaa tta tca gtt ctt tgt gat gca gaa gtg gcc ctc atc gtc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe	
35 40 45	

tcc agc aga ggg aga ctt tat gaa ttt gcc aac cac agc gtg aag agg	192
Ser Ser Arg Gly Arg Leu Tyr Glu Phe Ala Asn His Ser Val Lys Arg	
50 55 60	

acg att gag agg tac aag aag act tgc gtt gac aac aac cac gga ggg	240
Thr Ile Glu Arg Tyr Lys Lys Thr Cys Val Asp Asn Asn His Gly Gly	
65 70 75 80	

gcg ata tca gag tcc aat tct cag tat tgg caa cag gag gct ggt aaa	288
Ala Ile Ser Glu Ser Asn Ser Gln Tyr Trp Gln Gln Glu Ala Gly Lys	
85 90 95	

ctc aga caa cag att gac att ttg caa aat gca aat agg cat ttg atg	336
Leu Arg Gln Gln Ile Asp Ile Leu Gln Asn Ala Asn Arg His Leu Met	
100 105 110	

ggg gac ggg ctt aca gct ttg aac att aag gaa ctc aag caa ctt gag	384
Gly Asp Gly Leu Thr Ala Leu Asn Ile Lys Glu Leu Lys Gln Leu Glu	
115 120 125	

gtt cga ctt gaa aaa gga atc agc cga gtg cga tcc aaa aag aac gag	432
Val Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu	
130 135 140	

atg ttg ctt gaa gag atc gac atc atg cag aga agg gaa cac ata ctt 480
 Met Leu Leu Glu Glu Ile Asp Ile Met Gln Arg Arg Glu His Ile Leu
 145 150 155 160

atc cag gag aat gag att ctt cgc agc aag ata gcc gag tgt cag aat 528
 Ile Gln Glu Asn Glu Ile Leu Arg Ser Lys Ile Ala Glu Cys Gln Asn
 165 170 175

agc cac aac acg aac atg tta tca gct ccg gaa tat gat gca ctg ccc 576
 Ser His Asn Thr Asn Met Leu Ser Ala Pro Glu Tyr Asp Ala Leu Pro
 180 185 190

gca ttc gac tct cga aat ttc cta cat gca aat cta atc gat gcg gcc 624
 Ala Phe Asp Ser Arg Asn Phe Leu His Ala Asn Leu Ile Asp Ala Ala
 195 200 205

cat cac tat gca cat cag gaa caa aca acg ctt cag ctt ggc tga 669
 His His Tyr Ala His Gln Glu Gln Thr Thr Leu Gln Leu Gly
 210 215 220

acgttgaagc ggtggacgct taaaactcaa tcaaggcacc cgaaaaatat gctagtaacc 729

ttgaatgaga ttcagagtcg aaatattgcg aggcaagagc acaatggaag agatagctcc 789

tagtatgaat atggatttat gatattaaca tatggtttgt cagcttttaa tatagctgtt 849

tgaacaaaag aatacaacat attagctagt attttttttg cgcattgttat ctttctgttg 909

<210> 4

<211> 222

<212> PRT

<213> Pinus radiata

<400> 4

Met Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn
 1 5 10 15
 Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
 35 40 45
 Ser Ser Arg Gly Arg Leu Tyr Glu Phe Ala Asn His Ser Val Lys Arg
 50 55 60
 Thr Ile Glu Arg Tyr Lys Lys Thr Cys Val Asp Asn Asn His Gly Gly
 65 70 75 80
 Ala Ile Ser Glu Ser Asn Ser Gln Tyr Trp Gln Gln Glu Ala Gly Lys
 85 90 95

```

Leu Arg Gln Gln Ile Asp Ile Leu Gln Asn Ala Asn Arg His Leu Met
      100                      105                      110
Gly Asp Gly Leu Thr Ala Leu Asn Ile Lys Glu Leu Lys Gln Leu Glu
      115                      120                      125
Val Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu
      130                      135                      140
Met Leu Leu Glu Glu Ile Asp Ile Met Gln Arg Arg Glu His Ile Leu
145                      150                      155                      160
Ile Gln Glu Asn Glu Ile Leu Arg Ser Lys Ile Ala Glu Cys Gln Asn
      165                      170                      175
Ser His Asn Thr Asn Met Leu Ser Ala Pro Glu Tyr Asp Ala Leu Pro
      180                      185                      190
Ala Phe Asp Ser Arg Asn Phe Leu His Ala Asn Leu Ile Asp Ala Ala
      195                      200                      205
His His Tyr Ala His Gln Glu Gln Thr Thr Leu Gln Leu Gly
      210                      215                      220

```

<210> 5

<211> 1012

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(795)

<223> Arabidopsis thaliana ribonuclease (RNS2) mRNA,
complete cds

<300>

<301> Taylor, C B.

Bariola, P A.

delCardayre, S B.

Raines, R T.

Green, P J.

<302> RNS2: a senescence-associated RNase of Arabidopsis that
diverged from the S-RNases before speciation

<303> Proc. Natl. Acad. Sci. U.S.A.

<304> 90

<305> 11

<306> 5118-5122

<307> 1993

<308> Genbank

<309> 1994-10-30

<313> 1 TO 1012

<400> 5

```

atcgaattaa agtca atg gcg tca cgt tta tgt ctt ctc ctt ctc gtt gcg 51
      Met Ala Ser Arg Leu Cys Leu Leu Leu Leu Val Ala
            1              5              10

tgt atc gcc gga gca ttt gcc gga gac gtc atc gaa ctc aat cga tct 99
Cys Ile Ala Gly Ala Phe Ala Gly Asp Val Ile Glu Leu Asn Arg Ser
      15              20              25

cag agg gag ttc gat tat ttc gct cta tct ctt caa tgg cct gga acc 147
Gln Arg Glu Phe Asp Tyr Phe Ala Leu Ser Leu Gln Trp Pro Gly Thr
      30              35              40

tat tgc cgt gga act cgc cat tgt tgc tcc aaa aac gct tgc tgc aga 195
Tyr Cys Arg Gly Thr Arg His Cys Cys Ser Lys Asn Ala Cys Cys Arg
      45              50              55              60

ggc tcc gat gct cca act caa ttc aca att cat ggg tta tgg cct gac 243
Gly Ser Asp Ala Pro Thr Gln Phe Thr Ile His Gly Leu Trp Pro Asp
            65              70              75

tat aac gat ggt tgc tgg cct tca tgt tgt tat cga tct gac ttt aaa 291
Tyr Asn Asp Gly Ser Trp Pro Ser Cys Cys Tyr Arg Ser Asp Phe Lys
            80              85              90

gag aag gag att tca acg ttg atg gat ggt ctt gag aag tac tgg cct 339
Glu Lys Glu Ile Ser Thr Leu Met Asp Gly Leu Glu Lys Tyr Trp Pro
            95              100              105

agt ctc agt tgt ggt tct cca tca tca tgc aat ggt ggg aaa ggg tca 387
Ser Leu Ser Cys Gly Ser Pro Ser Ser Cys Asn Gly Gly Lys Gly Ser
            110              115              120

ttt tgg ggc cac gag tgg gag aaa cat ggg act tgt tct tct cct gtt 435
Phe Trp Gly His Glu Trp Glu Lys His Gly Thr Cys Ser Ser Pro Val
      125              130              135              140

ttt cat gat gag tat aat tac ttc ctt acc aca ctt aat ctc tac ttg 483
Phe His Asp Glu Tyr Asn Tyr Phe Leu Thr Thr Leu Asn Leu Tyr Leu
            145              150              155

aag cat aat gtc acg gat gtc ctt tat caa gct ggc tat gtt gct tcc 531
Lys His Asn Val Thr Asp Val Leu Tyr Gln Ala Gly Tyr Val Ala Ser
            160              165              170

aac agt gaa aag tat cct cta gga ggt atc gta aca gcc att cag aat 579
Asn Ser Glu Lys Tyr Pro Leu Gly Gly Ile Val Thr Ala Ile Gln Asn
            175              180              185

```

```

gca ttt cat atc acc cct gaa gtg gtt tgc aaa aga gat gca atc gat 627
Ala Phe His Ile Thr Pro Glu Val Val Cys Lys Arg Asp Ala Ile Asp
      190                195                200

gaa ata cgt ata tgc ttc tat aaa gat ttt aag ccc agg gac tgt gtt 675
Glu Ile Arg Ile Cys Phe Tyr Lys Asp Phe Lys Pro Arg Asp Cys Val
      205                210                215                220

ggg tca caa gat ttg aca tct aga aag tca tgc ccc aag tac gta agt 723
Gly Ser Gln Asp Leu Thr Ser Arg Lys Ser Cys Pro Lys Tyr Val Ser
              225                230                235

ttg ccg gaa tac acg cca tta gat ggt gaa gct atg gtt ctg aag atg 771
Leu Pro Glu Tyr Thr Pro Leu Asp Gly Glu Ala Met Val Leu Lys Met
              240                245                250

cca aca gaa aga gaa gct ctt tga atcggaag atgggagctt tggtatcttc 825
Pro Thr Glu Arg Glu Ala Leu
      255                260

tgagagacaa tacatacatg tctctgatgt tgtaacttta ctacaaaac ctataaagat 885

tggccttattt cgttctattg gatatgtatc atcattactg gtaaatacaag tttctttcta 945

ataatgtaga agatcagaaa atccataaga agatatcaac atttgagttc tatggtaaaa 1005

aaaaaaaaa 1012

```

<210> 6

<211> 259

<212> PRT

<213> Arabidopsis thaliana

<400> 6

```

Met Ala Ser Arg Leu Cys Leu Leu Leu Val Ala Cys Ile Ala Gly
  1          5          10          15
Ala Phe Ala Gly Asp Val Ile Glu Leu Asn Arg Ser Gln Arg Glu Phe
      20          25          30
Asp Tyr Phe Ala Leu Ser Leu Gln Trp Pro Gly Thr Tyr Cys Arg Gly
      35          40          45
Thr Arg His Cys Cys Ser Lys Asn Ala Cys Cys Arg Gly Ser Asp Ala
      50          55          60
Pro Thr Gln Phe Thr Ile His Gly Leu Trp Pro Asp Tyr Asn Asp Gly
      65          70          75          80
Ser Trp Pro Ser Cys Cys Tyr Arg Ser Asp Phe Lys Glu Lys Glu Ile
      85          90          95
Ser Thr Leu Met Asp Gly Leu Glu Lys Tyr Trp Pro Ser Leu Ser Cys

```

	100		105		110										
Gly	Ser	Pro	Ser	Ser	Cys	Asn	Gly	Gly	Lys	Gly	Ser	Phe	Trp	Gly	His
	115		120		125										
Glu	Trp	Glu	Lys	His	Gly	Thr	Cys	Ser	Ser	Pro	Val	Phe	His	Asp	Glu
	130		135		140										
Tyr	Asn	Tyr	Phe	Leu	Thr	Thr	Leu	Asn	Leu	Tyr	Leu	Lys	His	Asn	Val
145			150		155										
Thr	Asp	Val	Leu	Tyr	Gln	Ala	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Glu	Lys
	165		170		175										
Tyr	Pro	Leu	Gly	Gly	Ile	Val	Thr	Ala	Ile	Gln	Asn	Ala	Phe	His	Ile
	180		185		190										
Thr	Pro	Glu	Val	Val	Cys	Lys	Arg	Asp	Ala	Ile	Asp	Glu	Ile	Arg	Ile
	195		200		205										
Cys	Phe	Tyr	Lys	Asp	Phe	Lys	Pro	Arg	Asp	Cys	Val	Gly	Ser	Gln	Asp
	210		215		220										
Leu	Thr	Ser	Arg	Lys	Ser	Cys	Pro	Lys	Tyr	Val	Ser	Leu	Pro	Glu	Tyr
225			230		235										
Thr	Pro	Leu	Asp	Gly	Glu	Ala	Met	Val	Leu	Lys	Met	Pro	Thr	Glu	Arg
	245		250		255										

Glu Ala Leu

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<220>

<221> modified_base

<222> (3)

<223> i

<220>

<221> modified_base

<222> (6)

<223> i

<220>

<221> modified_base

<222> (9)

<223> i

<220>

<221> modified_base

<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

<400> 7

gcngtnagny cntcncccat

20

<210> 8

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<220>

<221> modified_base

<222> (6)

<223> i

<220>

<221> modified_base

<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

<400> 8

aaycgncarg tnacntt

17

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 9

cgcccttcttc aataaaccat ttcggcgctt

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 10

gacctgtcgg ttcgtagtat tttcaatcct

30

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 11

ttcgtcctcc attttgtgcg ctctccattc

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 12

gcactccact cttcctttat ttcttaccac

30

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 13

agttacttaa caatgcgcaa ccaaggc

27

<210> 14

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 14

ttgtgtacaa atcatggg

18

<210> 15

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 15

gtaagcccggt cacccatc

18

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 16

gaacaagatg gattgcacgc

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Made in lab

<400> 17

WO 00/55172

PCT/NZ00/00031

gaagaactcg tcaagaaggc

20